FIG. 1

```
           1                                                        56
Il6 human  MnsFStsaFgPVAFsLGLLLV1paAFPapvppgeDskDvaaPhRQpLTsSErIDkg
Il6 mouse  MkFLSaRdFhPVAF.LGLMLVttTAFPtsqvrRGDFtEdttPnRpVyTtSQ.VGg1
Il6 hhv8   McWFklWsL....L1VGsLLVsgT........RGKLpDapefeKDLLi......qr
 Consensus *               *  **

           57                                                      112
Il6 human  IrYILdgIsaLRKEtCNKsnMCeSskEALAENNLnLPkMaEkDGCFQsGFNEEtCL
Il6 mouse  IthVLWeIvEMRKELCNgnSdCmnndDALAENNLKLPeIqrnDGCYQtGYNQEiCL
Il6 hhv8   LnWMLWvIdEcfRDLCyRtGICkGilEpaAifhLKLPaInDtDhCgliGFNEtsCL
 Consensus     *  *       *     *       *   * **     * *   * *   **
                          ^     ^                      ^         ^

           113                                                     168
Il6 human  VKIitGLLEFEVYLEYLqNrF.EsSeEqARaVQMsTKvLIQFLQkkaKNLdaIttP
Il6 mouse  LKIssGLLEYhsYLEYMkNnLkDnkkDkARVLQrdTeTLIHIFnQEVKDLhKIvlP
Il6 hhv8   kKLadGFFEFEVlFkFLtteF.GkSvinvdVMELlTKTLgwdIQEELnkLtKthys
 Consensus  *   *  *                          *  *          *

           169                                                   223
Il6 human  dPttNASLLtKLQAQnQWLqdmTtHLILRSFkEFLqssLRaLRQM.........
Il6 mouse  tPisNAlLtDKLESQKEWLRtkTiQFILKSLEEFLkvtLRstRQt.........
Il6 hhv8   pPkfDrGLLGRLQGlKyWVRhfasfYVLsaMEkFagqaVRvLdsIpdvtpdvhdk
 Consensus  *     *   *     *        *     *     *
```

FIG. 2A

SEQUENCE LISTING

1.	Sequence characteristics:		
	1.1.	Length:	612 base pairs
	1.2.	Type:	Nucleic Acid
	1.3.	Strandedness:	Double stranded
	1.4.	Topology:	Linear
2.	Molecule type:		Genomic DNA
3.	Description:		Human herpesvirus 8 interleukin-6 gene
4.	Hypothetical:		No
5.	Anti-sense:		No
6.	Original source:		Kaposi Sarkoma from HIV positive donor
7.	Organism:		Human herpesvirus 8

FIG. 2 B

```
1    ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG
1      M   C   W   F   K   L   W   S   L   L   L   V   G   S   L
1    Met Cys Trp Phe Lys Leu Trp Seu Leu Leu Leu Val Gly Ser Leu

46   CTG GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT
16     L   V   S   G   T   R   G   K   L   P   D   A   P   E   F
16   Leu Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe

91   GAA AAG GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG
31     E   K   K   L   L   I   Q   R   L   N   W   M   L   W   V
31   Glu Lys Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val

136  ATC GAT GAA TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC
46     I   D   E   C   F   R   D   L   C   Y   R   T   G   I   C
46   Ile Asp Glu Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys

181  AAG GGT ATT CTA GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA
61     K   G   I   L   E   P   A   A   I   F   H   L   K   L   P
61   Lys Gly Ile Leu Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro

226  GCC ATC AAC GAT ACT GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG
76     A   I   N   D   T   D   H   C   G   L   I   G   F   N   E
76   Ala Ile Asn Asp Thr Asp His Cys Gly Leu Ile Gly Phe Asn Glu

271  ACT AGC TGC CTT AAA AAG CTC GCC GAT GGC TTT TTT GAA TTC GAG
91     T   S   C   L   K   K   L   A   D   G   F   F   E   F   E
91   Thr Ser Cys Leu Lys Lys Leu Ala Asp Gly Phe Phe Glu Phe Glu

316  GTG TTG TTT AAG TTT TTA ACG ACG GAG TTT GGA AAA TCA GTG ATA
106    V   L   F   K   F   L   T   T   E   F   G   K   S   V   I
106  Val Leu Phe Lys Phe Leu Thr Thr Glu Phe Gly Lys Ser Val Ile

361  AAC GTG GAC GTC ATG GAG CTT CTG ACG AAG ACC TTA GGA TGG GAC
121    N   V   D   V   M   E   L   L   T   K   T   L   G   W   D
121  Asn Val Asp Val Met Glu Leu Leu Thr Lys Thr Leu Gly Trp Asp

406  ATA CAG GAA GAG CTC AAT AAG CTG ACT AAG ACG CAC TAC AGT CCA
136    I   Q   E   E   L   N   K   L   T   K   T   H   Y   S   P
136  Ile Gln Glu Glu Leu Asn Lys Leu Thr Lys Thr His Tyr Ser Pro
```

FIG. 2C

```
451   CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG CTT CAG GGA CTT AAG
151     P   K   F   D   R   G   L   L   G   R   L   Q   G   L   K
151   Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg Leu Gln Gly Leu Lys

496   TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT CTG AGT GCA ATG
166     Y   W   V   R   H   F   A   S   F   Y   V   L   S   A   M
166   Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val Leu Ser Ala Met

541   GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC TCT ATC CCA
181     E   K   F   A   G   Q   A   V   R   V   L   D   S   I   P
181   Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp Ser Ile Pro

586   GAC GTG ACT CCT GAC GTC CAC GAT AAG
196     D   V   T   P   D   V   H   D   K
196   Asp Val Thr Pro Asp Val His Asp Lys
```